

## SEQUENCE LISTING



<110> Glaxo Group Ltd  
 Tate, Simon N  
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 Sanseau, P

<120> Novel Receptors

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<150> GB 9826359.3

<151> 1998-12-01

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<170> PatentIn Ver. 2.1

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 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro  
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 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro  
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Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu  
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 Lys Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp  
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495

Leu Gln Arg Arg Pro Ser Met Lys Thr Leu Phe Val Asp Ser Tyr Ser

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Glu Met Leu Phe Phe Leu Gln Ser Leu Phe Met Leu Ala Thr Val Val

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Leu Tyr Phe Ser His Leu Lys Glu Tyr Val Ala Ser Met Val Phe Ser

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540

Leu Ala Leu Gly Trp Thr Asn Met Leu Tyr Tyr Thr Arg Gly Phe Gln

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555

560

Gln Met Gly Ile Tyr Ala Val Met Ile Glu Lys Met Ile Leu Arg Asp

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570

575

Leu Cys Arg Phe Met Phe Val Tyr Ile Val Phe Leu Phe Gly Phe Ser

580

585

590

Thr Ala Val Val Thr Leu Ile Glu Asp Gly Lys Asn Asp Ser Leu Pro

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600

605

Ser Glu Ser Thr Ser His Arg Trp Arg Gly Pro Ala Cys Arg Pro Pro

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625

630

635

640

Phe Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu Asn Tyr Asp Phe

645

650

655

Lys Ala Val Phe Ile Ile Leu Leu Leu Ala Tyr Val Ile Leu Thr Tyr

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665

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B1

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Asp Asp Tyr Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Thr Thr  
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Trp Asn Thr Asn Val Gly Ile Ile Asn Glu Asp Pro Gly Asn Cys Glu  
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Gly Val Lys Arg Thr Leu Ser Phe Ser Leu Arg Ser Ser Arg Val Ser  
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Gly Arg His Trp Lys Asn Phe Ala Leu Val Pro Leu Leu Arg Glu Ala  
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Ser Ala Arg Asp Arg Gln Ser Ala Gln Pro Glu Glu Val Tyr Leu Arg  
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Val Leu Thr Ile Gln Arg Pro Gly Asp Gly Pro Ala Ser Val Arg Pro  
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Ser Ser Gln Asp Ser Val Ser Ala Gly Glu Lys Pro Pro Arg Leu Tyr  
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Asp Arg Arg Ser Ile Phe Asp Ala Val Ala Gln Ser Asn Cys Gln Glu  
115 120 125

Leu Glu Ser Leu Leu Pro Phe Leu Gln Arg Ser Lys Lys Arg Leu Thr  
130 135 140

Asp Ser Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu Lys  
145 150 155 160

Ala Met Leu Asn Leu His Asn Gly Gln Asn Asp Thr Ile Ala Leu Leu  
165 170 175

Leu Asp Val Ala Arg Lys Thr Asp Ser Leu Lys Gln Phe Val Asn Ala  
180 185 190

Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile Ala

B1

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 225                                      230                                      235                                      240  
 Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala Ala  
 245                                      250                                      255  
  
 Cys Thr Asn Gln Leu Ala Ile Val Lys Phe Leu Leu Gln Asn Ser Trp  
 260                                      265                                      270  
  
 Gln Pro Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val Leu  
 275                                      280                                      285  
  
 His Ala Leu Val Glu Val Ala Asp Asn Thr Val Asp Asn Thr Lys Phe  
 290                                      295                                      300  
  
 Val Thr Ser Met Tyr Asn Glu Ile Leu Ile Leu Gly Ala Lys Leu His  
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 Pro Thr Leu Lys Leu Glu Glu Ile Thr Asn Arg Lys Gly Leu Thr Pro  
 325                                      330                                      335  
  
 Leu Ala Leu Ala Ala Ser Ser Gly Lys Ile Gly Val Leu Ala Tyr Ile  
 340                                      345                                      350  
  
 Leu Gln Arg Glu Ile His Glu Pro Glu Cys Arg His Leu Ser Arg Lys  
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 Phe Thr Glu Trp Ala Tyr Gly Pro Val His Ser Ser Leu Tyr Asp Leu  
 370                                      375                                      380  
  
 Ser Cys Ile Asp Thr Cys Glu Lys Asn Ser Val Leu Glu Val Ile Ala  
 385                                      390                                      395                                      400



Tyr Ser Ser Ser Glu Thr Pro Asn Arg His Asp Met Leu Leu Val Glu  
 405 410 415

Pro Leu Asn Arg Leu Leu Gln Asp Lys Trp Asp Arg Phe Val Lys Arg  
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Ile Phe Tyr Phe Asn Phe Phe Val Tyr Cys Leu Tyr Met Ile Ile Phe  
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Thr Ala Ala Ala Tyr Tyr Arg Pro Val Glu Gly Leu Pro Pro Tyr Lys  
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 465 470 475 480

Ser Val Ser Gly Gly Val Tyr Phe Phe Phe Arg Gly Ile Gln Tyr Phe  
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Leu Gln Arg Arg Pro Ser Leu Lys Ser Leu Phe Val Asp Ser Tyr Ser  
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Glu Ile Leu Phe Phe Val Gln Ser Leu Phe Met Leu Val Ser Val Val  
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Leu Tyr Phe Ser Gln Arg Lys Glu Tyr Val Ala Ser Met Val Phe Ser  
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 545 550 555 560

Gln Met Gly Ile Tyr Ala Val Met Ile Glu Lys Met Ile Leu Arg Asp  
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Thr Ala Val Val Thr Leu Ile Glu Asp Gly Lys Asn Asn Ser Leu Pro  
 595 600 605

B1

Met Glu Ser Thr Pro His Lys Cys Arg Gly Ser Ala Cys Lys Pro Gly  
610 615 620

Asn Ser Tyr Asn Ser Leu Tyr Ser Thr Cys Leu Glu Leu Phe Lys Phe  
625 630 635 640

Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu Asn Tyr Asp Phe Lys  
645 650 655  
Ala Val Phe Ile Ile Leu Leu Leu Ala Tyr Val Ile Leu Thr Tyr Ile  
660 665 670

Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr Val Asn Lys  
675 680 685

Ile Ala Gln Glu Ser Lys Asn Ile Trp Lys Leu Gln Arg Ala Ile Thr  
690 695 700

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705 710 715 720

Arg Ser Gly Lys Leu Leu Gln Val Gly Phe Thr Pro Asp Gly Lys Asp  
725 730 735

Asp Tyr Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Thr Thr Trp  
740 745 750

Asn Thr Asn Val Gly Ile Ile Asn Glu Asp Pro Gly Asn Cys Glu Gly  
755 760 765

Val Lys Arg Thr Leu Ser Phe Ser Leu Arg Ser Gly Arg Val Ser Gly  
770 775 780

Arg Asn Trp Lys Asn Phe Ala Leu Val Pro Leu Leu Arg Asp Ala Ser  
785 790 795 800

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805

810

815

Tyr Thr Gly Ser Leu Lys Pro Glu Asp Ala Glu Val Phe Lys Asp Ser

820

825

830

Met Val Pro Gly Glu Lys

835

&lt;210&gt; 4

&lt;211&gt; 4118

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (686) .. (3577)

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gagtgtgtgc aggccaggga gggctttcca gaggagccca gttgagctgg aacaccagtg 180

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ggttcatcat gacagtgttt gatgaggaaa aggactgccg gcctacacag caagtccaca 360

tggattttct gagcccctcc tgtgcctgaa gcccacgggt aatggttctg ccttagcagg 420

tgcttaccac gtgccaggca ctgcactgca ctggccactg gactgcatgt tctgtccatg 480

aggcttggat atccccatct tacagatcag gaagctgagg ctatgaaatg tcgacttgct 540

B1

caatgtcatg gaatgactaa gtgtggagcc tggatttgaa cttggctctc tggggctcca 600

aagctggctt tcttggtcag cagtaggggc tgggatccaa gtatgggggc ccagcttgac 660

cctgaagtcc accctctttc agcta atg ccc agg gta gtt gga cct ggg gcc 712

Met Pro Arg Val Val Gly Pro Gly Ala

1

5

B1

aat ttg tgt ttc ,cag gtt cgt gaa aga ggc tcc tgt tgc agt tcc cgc 760  
 Asn Leu Cys Phe Gln Val Arg Glu Arg Gly Ser Cys Cys Ser Ser Arg  
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ctg agg ctg gcg gcc aac cac atc tgg gag tgg cct ccc tgt gcc cct 808  
 Leu Arg Leu Ala Ala Asn His Ile Trp Glu Trp Pro Pro Cys Ala Pro  
 30 35 40

gtc att aca acg gtg gct ttg aag cag ctg gca gca ctg ctg ctt gtc 856  
 Val Ile Thr Thr Val Ala Leu Lys Gln Leu Ala Ala Leu Leu Leu Val  
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cac gtg gga ggg ggc ttc ctg gag ccc ccg ccc ctg gcc ggg ttc tgc 904  
 His Val Gly Gly Gly Phe Leu Glu Pro Pro Pro Leu Ala Gly Phe Cys  
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ctg act ccc ctt tca ttc cct tgc agg ctg agc agt gca gac ggg cct 952  
 Leu Thr Pro Leu Ser Phe Pro Cys Arg Leu Ser Ser Ala Asp Gly Pro  
 75 80 85

ggg gca ggc atg gcg gat tcc agc gaa ggc ccc cgc gcg ggg ccc ggg 1000  
 Gly Ala Gly Met Ala Asp Ser Ser Glu Gly Pro Arg Ala Gly Pro Gly  
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gag gtg gct gag ctc ccc ggg gat gag agt ggc acc cca ggt ggg gag 1048  
 Glu Val Ala Glu Leu Pro Gly Asp Glu Ser Gly Thr Pro Gly Gly Glu  
 110 115 120

gct ttt cct ctc tcc tcc ctg gcc aat ctg ttt gag ggg gag gat ggc 1096  
 Ala Phe Pro Leu Ser Ser Leu Ala Asn Leu Phe Glu Gly Glu Asp Gly  
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tcc ctt tcg ccc tca ccg gct gat gcc agt cgc cct gct ggc cca ggc 1144  
 Ser Leu Ser Pro Ser Pro Ala Asp Ala Ser Arg Pro Ala Gly Pro Gly  
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B1

gat ggg cga cca aat ctg cgc atg aag ttc cag ggc gcc ttc cgc aag 1192  
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 155 160 165

ggg gtg ccc aac ccc atc gat ctg ctg gag tcc acc cta tat gag tcc 1240  
 Gly Val Pro Asn Pro Ile Asp Leu Leu Glu Ser Thr Leu Tyr Glu Ser  
 170 175 180 185

tcg gtg gtg cct ggg ccc aag aaa gca ccc atg gac tca ctg ttt gac 1288  
 Ser Val Val Pro Gly Pro Lys Lys Ala Pro Met Asp Ser Leu Phe Asp  
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tac ggc acc tat cgt cac cac tcc agt gac aac aag agg tgg agg aag 1336  
 Tyr Gly Thr Tyr Arg His His Ser Ser Asp Asn Lys Arg Trp Arg Lys  
 205 210 215

B1 aag atc ata gag aag cag ccg cag agc ccc aaa gcc cct gcc cct cag 1384  
 Lys Ile Ile Glu Lys Gln Pro Gln Ser Pro Lys Ala Pro Ala Pro Gln  
 220 225 230

ccg ccc ccc atc ctc aaa gtc ttc aac cgg cct atc ctc ttt gac atc 1432  
 Pro Pro Pro Ile Leu Lys Val Phe Asn Arg Pro Ile Leu Phe Asp Ile  
 235 240 245

gtg tcc cgg ggc tcc act gct gac ctg gac ggg ctg ctc cca ttc ttg 1480  
 Val Ser Arg Gly Ser Thr Ala Asp Leu Asp Gly Leu Leu Pro Phe Leu  
 250 255 260 265

ctg acc cac aag aaa cgc cta act gat gag gag ttt cga gag cca tct 1528  
 Leu Thr His Lys Lys Arg Leu Thr Asp Glu Glu Phe Arg Glu Pro Ser  
 270 275 280

acg ggg aag acc tgc ctg ccc aag gcc ttg ctg aac ctg agc aat ggc 1576  
 Thr Gly Lys Thr Cys Leu Pro Lys Ala Leu Leu Asn Leu Ser Asn Gly  
 285 290 295

cgc aac gac acc atc cct gtg ctg ctg gac atc gcg gag cgc acc ggc 1624  
 Arg Asn Asp Thr Ile Pro Val Leu Leu Asp Ile Ala Glu Arg Thr Gly  
 300 305 310

aac atg cgg gag ttc att aac tcg ccc ttc cgt gac atc tac tat cga 1672  
 Asn Met Arg Glu Phe Ile Asn Ser Pro Phe Arg Asp Ile Tyr Tyr Arg  
 315 320 325

ggt cag aca gcc ctg cac atc gcc att gag cgt cgc tgc aaa cac tac 1720  
 Gly Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Cys Lys His Tyr  
 330 335 340 345

gtg gaa ctt ctc gtg gcc cag gga gct gat gtc cac gcc cag gcc cgt 1768  
 Val Glu Leu Leu Val Ala Gln Gly Ala Asp Val His Ala Gln Ala Arg  
 350 355 360

131 ggg cgc ttc ttc cag ccc aag gat gag ggg ggc tac ttc tac ttt ggg 1816  
 Gly Arg Phe Phe Gln Pro Lys Asp Glu Gly Gly Tyr Phe Tyr Phe Gly  
 365 370 375

gag ctg ccc ctg tcg ctg gct gcc tgc acc aac cag ccc cac att gtc 1864  
 Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Pro His Ile Val  
 380 385 390

aac tac ctg acg gag aac ccc cac aag aag gcg gac atg cgg cgc cag 1912  
 Asn Tyr Leu Thr Glu Asn Pro His Lys Lys Ala Asp Met Arg Arg Gln  
 395 400 405

gac tcg cga ggc aac aca gtg ctg cat gcg ctg gtg gcc att gct gac 1960  
 Asp Ser Arg Gly Asn Thr Val Leu His Ala Leu Val Ala Ile Ala Asp  
 410 415 420 425

aac acc cgt gag aac acc aag ttt gtt acc aag atg tac gac ctg ctg 2008  
 Asn Thr Arg Glu Asn Thr Lys Phe Val Thr Lys Met Tyr Asp Leu Leu  
 430 435 440

ctg ctc aag tgt gcc cgc ctc ttc ccc gac agc aac ctg gag gcc gtg 2056  
 Leu Leu Lys Cys Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val  
 445 450 455

ctc aac aac gac ggc ctc tcg ccc ctc atg atg gct gcc aag acg ggc 2104  
 Leu Asn Asn Asp Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly  
 460 465 470

aag att ggg atc ttt cag cac atc atc cgg cgg gag gtg acg gat gag 2152  
 Lys Ile Gly Ile Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu  
 475 480 485

gac aca cgg cac ctg tcc cgc aag tcc aag gac tgg gcc tat ggg cca 2200  
 Asp Thr Arg His Leu Ser Arg Lys Ser Lys Asp Trp Ala Tyr Gly Pro  
 490 495 500 505

B1 gtg tat tcc tcg ctt tat gac ctc tcc tcc ctg gac acg tgt ggg gaa 2248  
 Val Tyr Ser Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu  
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gag gcc tcc gtg ctg gag atc ctg gtg tac aac agc aag att gag aac 2296  
 Glu Ala Ser Val Leu Glu Ile Leu Val Tyr Asn Ser Lys Ile Glu Asn  
 525 530 535

cgc cac gag atg ctg gct gtg gag ccc atc aat gaa ctg ctg cgg gac 2344  
 Arg His Glu Met Leu Ala Val Glu Pro Ile Asn Glu Leu Leu Arg Asp  
 540 545 550

aag tgg cgg aag ttc ggg gcc gtc tcc ttc tac atc aac gtg gtc tcc 2392  
 Lys Trp Arg Lys Phe Gly Ala Val Ser Phe Tyr Ile Asn Val Val Ser  
 555 560 565

tac ctg tgt gcc atg gtt atc ttc act ctc acc gcc tac tac cag ccg 2440  
 Tyr Leu Cys Ala Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro  
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ctg gag ggc aca ccg ccg tac cct tac cgc acc acg gtg gac tac ctg 2488  
 Leu Glu Gly Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu  
                     590                    595                    600

cgg ctg gct ggc gag gtc att acg ctc ttc act ggg gtc ctg ttc ttc 2536  
 Arg Leu Ala Gly Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe  
                     605                    610                    615

ttc acc aac atc aaa gac ttg ttc atg aag aaa tgc cct gga gtg aat 2584  
 Phe Thr Asn Ile Lys Asp Leu Phe Met Lys Lys Cys Pro Gly Val Asn  
                     620                    625                    630

tct ctc ttc att gat ggc tcc ttc cag ctg ctc tac ttc atc tac tct 2632  
 Ser Leu Phe Ile Asp Gly Ser Phe Gln Leu Leu Tyr Phe Ile Tyr Ser  
                     635                    640                    645

gtc ctg gtg atc gtc tca gca gcc ctc tac ctg gca ggg atc gag gcc 2680  
 Val Leu Val Ile Val Ser Ala Ala Leu Tyr Leu Ala Gly Ile Glu Ala  
 650                    655                    660                    665

tac ctg gcc atg atg gtc ttt gcc ctg gtc ctg ggc tgg atg aat gcc 2728  
 Tyr Leu Ala Met Met Val Phe Ala Leu Val Leu Gly Trp Met Asn Ala  
                     670                    675                    680

ctt tac ttc acc cgt ggg ctg aag ctg acg ggg acc tat agc atc atg 2776  
 Leu Tyr Phe Thr Arg Gly Leu Lys Leu Thr Gly Thr Tyr Ser Ile Met  
                     685                    690                    695

atc cag aag att ctc ttc aag gac ctt ttc cga ttc ctg ctc gtc tac 2824  
 Ile Gln Lys Ile Leu Phe Lys Asp Leu Phe Arg Phe Leu Leu Val Tyr  
                     700                    705                    710

ttg ctc ttc atg atc ggc tac gct tca gcc ctg gtc tcc ctc ctg aac 2872  
 Leu Leu Phe Met Ile Gly Tyr Ala Ser Ala Leu Val Ser Leu Leu Asn  
                     715                    720                    725

B1

ccg tgt gcc aac atg aag gtg tgc aat gag gac cag acc aac tgc aca 2920  
 Pro Cys Ala Asn Met Lys Val Cys Asn Glu Asp Gln Thr Asn Cys Thr  
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gtg ccc act tac ccc tcg tgc cgt gac agc gag acc ttc agc acc ttc 2968  
 Val Pro Thr Tyr Pro Ser Cys Arg Asp Ser Glu Thr Phe Ser Thr Phe  
 750 755 760

ctc ctg gac ctg ttt aag ctg acc atc ggc atg ggc gac ctg gag atg 3016  
 Leu Leu Asp Leu Phe Lys Leu Thr Ile Gly Met Gly Asp Leu Glu Met  
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ctg agc agc acc aag tac ccc gtg gtc ttc atc atc ctg ctg gtg acc 3064  
 Leu Ser Ser Thr Lys Tyr Pro Val Val Phe Ile Ile Leu Leu Val Thr  
 780 785 790

B1 tac atc atc ctc acc tct gtg ctg ctc ctc aac atg ctc att gcc ctc 3112  
 Tyr Ile Ile Leu Thr Ser Val Leu Leu Leu Asn Met Leu Ile Ala Leu  
 795 800 805

atg ggc gag aca gtg ggc cag gtc tcc aag gag agc aag cac atc tgg 3160  
 Met Gly Glu Thr Val Gly Gln Val Ser Lys Glu Ser Lys His Ile Trp  
 810 815 820 825

aag ctg cag tgg gcc acc acc atc ctg gac att gag cgc tcc ttc ccc 3208  
 Lys Leu Gln Trp Ala Thr Thr Ile Leu Asp Ile Glu Arg Ser Phe Pro  
 830 835 840

gta ttc ctg agg aag gcc ttc cgc tct ggg gag atg gtc acc gtg ggc 3256  
 Val Phe Leu Arg Lys Ala Phe Arg Ser Gly Glu Met Val Thr Val Gly  
 845 850 855

aag agc tcg gac ggc act cct gac cgc agg tgg tgc ttc agg gtg gat 3304  
 Lys Ser Ser Asp Gly Thr Pro Asp Arg Arg Trp Cys Phe Arg Val Asp  
 860 865 870

gag gtg aac tgg tct cac tgg aac cag aac ttg ggc atc atc aac gag 3352  
 Glu Val Asn Trp Ser His Trp Asn Gln Asn Leu Gly Ile Ile Asn Glu  
 875 880 885

gac ccg ggc aag aat gag acc tac cag tat tat ggc ttc tcg cat acc 3400  
 Asp Pro Gly Lys Asn Glu Thr Tyr Gln Tyr Tyr Gly Phe Ser His Thr  
 890 895 900 905

gtg ggc cgc ctc cgc agg gat cgc tgg tcc tcg gtg gta ccc cgc gtg 3448  
 Val Gly Arg Leu Arg Arg Asp Arg Trp Ser Ser Val Val Pro Arg Val  
 910 915 920

gtg gaa ctg aac aag aac tcg aac ccg gac gag gtg gtg gtg cct ctg 3496  
 Val Glu Leu Asn Lys Asn Ser Asn Pro Asp Glu Val Val Val Pro Leu  
 925 930 935

B1 gag agc atg ggg aac ccc cgc tgc gat ggc cac cag cag ggt tac ccc 3544  
 Asp Ser Met Gly Asn Pro Arg Cys Asp Gly His Gln Gln Gly Tyr Pro  
 940 945 950

cgc aag tgg agg act gat gac gcc ccg ctc tag ggactgcagc ccagccccag 3597  
 Arg Lys Trp Arg Thr Asp Asp Ala Pro Leu  
 955 960

cttctctgcc cactcatttc tagtccagcc gcatttcagc agtgccttct ggggtgtccc 3657

cccacaccct gctttggccc cagaggcgag ggaccagtgg aggtgccagg gagggcccag 3717

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<212> PRT

<213> Homo sapiens

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Glu Arg Gly Ser Cys Cys Ser Ser Arg Leu Arg Leu Ala Ala Asn His  
20 25 30

Ile Trp Glu Trp Pro Pro Cys Ala Pro Val Ile Thr Thr Val Ala Leu  
35 40 45

Lys Gln Leu Ala Ala Leu Leu Leu Val His Val Gly Gly Gly Phe Leu  
50 55 60

Glu Pro Pro Pro Leu Ala Gly Phe Cys Leu Thr Pro Leu Ser Phe Pro  
65 70 75 80

Cys Arg Leu Ser Ser Ala Asp Gly Pro Gly Ala Gly Met Ala Asp Ser  
85 90 95

Ser Glu Gly Pro Arg Ala Gly Pro Gly Glu Val Ala Glu Leu Pro Gly  
100 105 110

Asp Glu Ser Gly Thr Pro Gly Gly Glu Ala Phe Pro Leu Ser Ser Leu  
115 120 125

Ala Asn Leu Phe Glu Gly Glu Asp Gly Ser Leu Ser Pro Ser Pro Ala

130                                      135                                      140  
 Asp Ala Ser Arg Pro Ala Gly Pro Gly Asp Gly Arg Pro Asn Leu Arg  
 145                                      150                                      155                                      160  
 Met Lys Phe Gln Gly Ala Phe Arg Lys Gly Val Pro Asn Pro Ile Asp  
                                     165                                      170                                      175  
 Leu Leu Glu Ser Thr Leu Tyr Glu Ser Ser Val Val Pro Gly Pro Lys  
                                     180                                      185                                      190  
 Lys Ala Pro Met Asp Ser Leu Phe Asp Tyr Gly Thr Tyr Arg His His  
                                     195                                      200                                      205  
 Ser Ser Asp Asn Lys Arg Trp Arg Lys Lys Ile Ile Glu Lys Gln Pro  
                                     210                                      215                                      220  
 Gln Ser Pro Lys Ala Pro Ala Pro Gln Pro Pro Pro Ile Leu Lys Val  
 225                                      230                                      235                                      240  
 Phe Asn Arg Pro Ile Leu Phe Asp Ile Val Ser Arg Gly Ser Thr Ala  
                                     245                                      250                                      255  
 Asp Leu Asp Gly Leu Leu Pro Phe Leu Leu Thr His Lys Lys Arg Leu  
                                     260                                      265                                      270  
 Thr Asp Glu Glu Phe Arg Glu Pro Ser Thr Gly Lys Thr Cys Leu Pro  
                                     275                                      280                                      285  
 Lys Ala Leu Leu Asn Leu Ser Asn Gly Arg Asn Asp Thr Ile Pro Val  
                                     290                                      295                                      300  
 Leu Leu Asp Ile Ala Glu Arg Thr Gly Asn Met Arg Glu Phe Ile Asn  
 305                                      310                                      315                                      320  
 Ser Pro Phe Arg Asp Ile Tyr Tyr Arg Gly Gln Thr Ala Leu His Ile  
                                     325                                      330                                      335

B1

Ala Ile Glu Arg Arg Cys Lys His Tyr Val Glu Leu Leu Val Ala Gln  
 340 345 350

Gly Ala Asp Val His Ala Gln Ala Arg Gly Arg Phe Phe Gln Pro Lys  
 355 360 365

Asp Glu Gly Gly Tyr Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala  
 370 375 380

Ala Cys Thr Asn Gln Pro His Ile Val Asn Tyr Leu Thr Glu Asn Pro  
 385 390 395 400

His Lys Lys Ala Asp Met Arg Arg Gln Asp Ser Arg Gly Asn Thr Val  
 405 410 415

Leu His Ala Leu Val Ala Ile Ala Asp Asn Thr Arg Glu Asn Thr Lys  
 420 425 430

Phe Val Thr Lys Met Tyr Asp Leu Leu Leu Lys Cys Ala Arg Leu  
 435 440 445

Phe Pro Asp Ser Asn Leu Glu Ala Val Leu Asn Asn Asp Gly Leu Ser  
 450 455 460

Pro Leu Met Met Ala Ala Lys Thr Gly Lys Ile Gly Ile Phe Gln His  
 465 470 475 480

Ile Ile Arg Arg Glu Val Thr Asp Glu Asp Thr Arg His Leu Ser Arg  
 485 490 495

Lys Ser Lys Asp Trp Ala Tyr Gly Pro Val Tyr Ser Ser Leu Tyr Asp  
 500 505 510

Leu Ser Ser Leu Asp Thr Cys Gly Glu Glu Ala Ser Val Leu Glu Ile  
 515 520 525

Leu Val Tyr Asn Ser Lys Ile Glu Asn Arg His Glu Met Leu Ala Val

B1

530                                      535                                      540  
 Glu Pro Ile Asn Glu Leu Leu Arg Asp Lys Trp Arg Lys Phe Gly Ala  
 545                                      550                                      555                                      560  
 Val Ser Phe Tyr Ile Asn Val Val Ser Tyr Leu Cys Ala Met Val Ile  
                                     565                                      570                                      575  
  
 Phe Thr Leu Thr Ala Tyr Tyr Gln Pro Leu Glu Gly Thr Pro Pro Tyr  
                                     580                                      585                                      590  
  
 Pro Tyr Arg Thr Thr Val Asp Tyr Leu Arg Leu Ala Gly Glu Val Ile  
                                     595                                      600                                      605  
  
 Thr Leu Phe Thr Gly Val Leu Phe Phe Phe Thr Asn Ile Lys Asp Leu  
                                     610                                      615                                      620  
  
 Phe Met Lys Lys Cys Pro Gly Val Asn Ser Leu Phe Ile Asp Gly Ser  
 625                                      630                                      635                                      640  
  
 Phe Gln Leu Leu Tyr Phe Ile Tyr Ser Val Leu Val Ile Val Ser Ala  
                                     645                                      650                                      655  
  
 Ala Leu Tyr Leu Ala Gly Ile Glu Ala Tyr Leu Ala Met Met Val Phe  
                                     660                                      665                                      670  
  
 Ala Leu Val Leu Gly Trp Met Asn Ala Leu Tyr Phe Thr Arg Gly Leu  
                                     675                                      680                                      685  
  
 Lys Leu Thr Gly Thr Tyr Ser Ile Met Ile Gln Lys Ile Leu Phe Lys  
                                     690                                      695                                      700  
  
 Asp Leu Phe Arg Phe Leu Leu Val Tyr Leu Leu Phe Met Ile Gly Tyr  
 705                                      710                                      715                                      720  
  
 Ala Ser Ala Leu Val Ser Leu Leu Asn Pro Cys Ala Asn Met Lys Val  
                                     725                                      730                                      735

B1

Cys Asn Glu Asp Gln Thr Asn Cys Thr Val Pro Thr Tyr Pro Ser Cys  
 740 745 750

Arg Asp Ser Glu Thr Phe Ser Thr Phe Leu Leu Asp Leu Phe Lys Leu  
 755 760 765

Thr Ile Gly Met Gly Asp Leu Glu Met Leu Ser Ser Thr Lys Tyr Pro  
 770 775 780

Val Val Phe Ile Ile Leu Leu Val Thr Tyr Ile Ile Leu Thr Ser Val  
 785 790 795 800

Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu Thr Val Gly Gln  
 805 810 815

Val Ser Lys Glu Ser Lys His Ile Trp Lys Leu Gln Trp Ala Thr Thr  
 820 825 830

Ile Leu Asp Ile Glu Arg Ser Phe Pro Val Phe Leu Arg Lys Ala Phe  
 835 840 845

Arg Ser Gly Glu Met Val Thr Val Gly Lys Ser Ser Asp Gly Thr Pro  
 850 855 860

Asp Arg Arg Trp Cys Phe Arg Val Asp Glu Val Asn Trp Ser His Trp  
 865 870 875 880

Asn Gln Asn Leu Gly Ile Ile Asn Glu Asp Pro Gly Lys Asn Glu Thr  
 885 890 895

Tyr Gln Tyr Tyr Gly Phe Ser His Thr Val Gly Arg Leu Arg Arg Asp  
 900 905 910

Arg Trp Ser Ser Val Val Pro Arg Val Val Glu Leu Asn Lys Asn Ser  
 915 920 925

Asn Pro Asp Glu Val Val Val Pro Leu Asp Ser Met Gly Asn Pro Arg  
 930 935 940



Cys Asp Gly His Gln Gln Gly Tyr Pro Arg Lys Trp Arg Thr Asp Asp  
 945 950 955 960

Ala Pro Leu

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<211> 764

<212> PRT

<213> Homo sapiens

<400> 6

Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp  
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Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe  
 20 25 30

B1 Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg  
 35 40 45

Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr  
 50 55 60

Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe  
 65 70 75 80

Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu  
 85 90 95

Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu  
 100 105 110

Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys  
 115 120 125

Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp

Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn  
 340 345 350

Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His  
 355 360 365

Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp  
 370 375 380

Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile  
 385 390 395 400

Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys  
 405 410 415

Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu  
 420 425 430

Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr Leu Leu Val  
 435 440 445

Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser  
 450 455 460

Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu  
 465 470 475 480

Thr Val Val Ser Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu  
 485 490 495

Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr  
 500 505 510

Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln  
 515 520 525

Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val  
 530 535 540

B1

130						135						140					
Ser	Gly	Asn	Pro	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr		
145					150					155					160		
Tyr	Arg	Gly	His	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu		
				165					170					175			
Gln	Cys	Val	Lys	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg		
			180					185					190				
Ala	Cys	Gly	Arg	Phe	Phe	Gln	Lys	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe		
		195					200						205				
Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val		
	210					215						220					
Val	Ser	Tyr	Leu	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala		
225					230					235					240		
Thr	Asp	Ser	Gln	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser		
				245					250					255			
Asp	Asn	Ser	Ala	Glu	Asn	Ile	Ala	Leu	Val	Thr	Ser	Met	Tyr	Asp	Gly		
			260				265						270				
Leu	Leu	Gln	Ala	Gly	Ala	Arg	Leu	Cys	Pro	Thr	Val	Gln	Leu	Glu	Asp		
		275					280						285				
Ile	Arg	Asn	Leu	Gln	Asp	Leu	Thr	Pro	Leu	Lys	Leu	Ala	Ala	Lys	Glu		
	290					295						300					
Gly	Lys	Ile	Glu	Ile	Phe	Arg	His	Ile	Leu	Gln	Arg	Glu	Phe	Ser	Gly		
305					310					315					320		
Leu	Ser	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Cys	Tyr	Gly	Pro	Val		
				325					330						335		

Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala  
 545 550 555 560

Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln  
 565 570 575

Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly  
 580 585 590

Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly  
 595 600 605

Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu  
 610 615 620

Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met  
 625 630 635 640

Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser  
 645 650 655

Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu  
 660 665 670

Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu  
 675 680 685

Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe  
 690 695 700

Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr  
 705 710 715 720

Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn  
 725 730 735

Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu

B1

37

740

745

750

B1

Glu Asn Tyr Val Pro Val Gln Leu Leu Gln Ser Asn

755

760

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aggcccactc ggtgaacttc

20

<210> 21

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gacgagcatg tacaatgaga

20

B1

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20

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32

B1

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10

15

Asp Ser Glu Glu Ala Ser Cys

20

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&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
sequence

&lt;400&gt; 28

Cys Gly Ser Leu Lys Pro Glu Asp Ala Glu Val Phe Lys Asp Ser Met

1

5

10

15

Val Pro Gly Glu Lys

20

&lt;210&gt; 29

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 29

atggccacca gcagggttac

20

&lt;210&gt; 30

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

B1

<223> Description of Artificial Sequence: Primer

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18

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41

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23

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B1



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18

<210> 39

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acaagaaggc ggacatgcgg

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B1

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<212> DNA

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<220>

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atctcgtggc ggttctcaat

20

PAGE:  
02/14/2003

1

ERROR LISTING  
PATENT APPLICATION

DATE:  
TIME:

12:07:35

INPUT SEQ: A:\Pg3606SEQLIST.txt

L:1727 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:40

B1